

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 7

**Amendments to the Claims**

This listing of claims will replace all prior versions, and listing, of claims in the application.

**Listing of Claims:**

1-191        canceled

192. (New) An isolated protein having a first protein which is FHOS or a homologue or derivative or fragment thereof, interacting with a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof, wherein the interaction is through a complex or covalent bond, or any other intermolecular interaction.

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 8

193. (new) The isolated protein complex of Claim 192, wherein said first protein consists of an amino acid sequence set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117, said second protein consists of an amino acid sequence selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138

194. (new) The isolated protein complex of Claim 192, wherein said first protein is a hybrid protein containing the complete amino acid sequence of FHOS.

195. (new) The isolated protein complex of Claim 192, wherein said second protein is a hybrid protein containing the complete amino acid sequence of a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g,

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 9

m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK.

196. (new) The isolated protein complex of Claim 192, wherein said first protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, and 117

197. (new) The isolated protein complex of Claim 192, wherein said second protein comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138.

198. (new) A method for making the protein complex of claim 192, comprising the step of providing said first protein and said second protein under conditions such that said first and second proteins contact each other.

199. (new) A method for detecting, in a sample, a protein complex containing FHOS and a polypeptide selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL , and mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9,

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 10

mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon,  
BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015,  
PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241),  
SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3,  
mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-  
3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX,  
mPRKCABP and mMYLK comprising:

contacting said sample with an antibody selected from the group  
consisting of an antibody specific to said protein complex, an antibody specific to  
FHOS and an antibody specific to a protein selected from the group consisting of  
mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF,  
mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-  
pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633,  
KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik,  
mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon,  
BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015,  
PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241),  
SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3,  
mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-  
3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX,  
mPRKCABP and mMYLK.

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 11

200. (new) A method for selecting modulators of a protein complex formed between a first protein which is FHOS or a homologue or derivative or fragment thereof and a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or a derivative or a fragment thereof, comprising:

providing the protein complex;

contacting said protein complex with a test compound; and

determining binding of the test compound with said protein complex.

201. (new) The method of Claim 200 wherein said test compound is provided in a phage display library.

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 12

202. (new) The method of Claim 200, wherein said test compound is provided in a combinatorial library.

203. (new) The method of Claim 200, wherein at least one of said first and second proteins are provided in the protein complex as a hybrid protein having a detectable tag fused thereto.

204. (new) A method for determining whether a compound is capable of modulating an interaction between a first polypeptide and a second polypeptide, said first polypeptide being FHOS or a homologue or derivative or fragment thereof and said second polypeptide being selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 13

3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP, mMYLK or a homologue or derivative or fragment thereof, said method comprising:

(a) expressing in an isolated host cell in the presence of a test compound, a first hybrid protein having a DNA binding domain fused to said first polypeptide, a second hybrid protein having a transcription-activating domain fused to said second polypeptide and a reporter gene, wherein the expression of the reporter gene is dependent on the interaction between the first polypeptide and the second polypeptide; and

(b) detecting the expression of said reporter gene.

205. (new) The isolated host cell of Claim 204, wherein said first protein consists of an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 and said second protein consists of an amino acid sequence selected from the group consisting of any of SEQ ID NOS: 4-26, 55- 86, and 118-138;

206. (new) The isolated host cell of Claim 204, wherein said first protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117.

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 14

207. (new) The isolated host cell of Claim 204, wherein said cell is a yeast cell.

208. (new) The isolated host cell of Claim 204, wherein said cell is a mammalian cell.

209. (new) A method for modulating the function or activity of a protein complex in cells of a specific tissue of a mammal, said protein complex having a first protein which is FHOS or a homologue or derivative or fragment thereof interacting with a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof, said method comprising:

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 15

delivering to the specific tissue, a selected compound for modulating the function or activity of said protein complex.

210. The method of Claim 209, wherein said compound is an antibody.

211. A method for screening to identify compounds that activate or that inhibit an activity of a protein complex formed between a first protein which is FHOS or a homologue or derivative or fragment thereof and a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK, or a homologue or a derivative or a fragment thereof, the method comprising:

Applicant: Takeshi SAKAMOTO, et al.

U.S.S.N. 10/805,684

Preliminary Amendment

Page 16

(a) measuring the activity of said protein complex in the presence of a candidate compound;

(b) measuring the activity of said protein complex in the absence of the candidate compound; and

(c) detecting the effect of the candidate compound by comparing the activity in (a) and (b)..